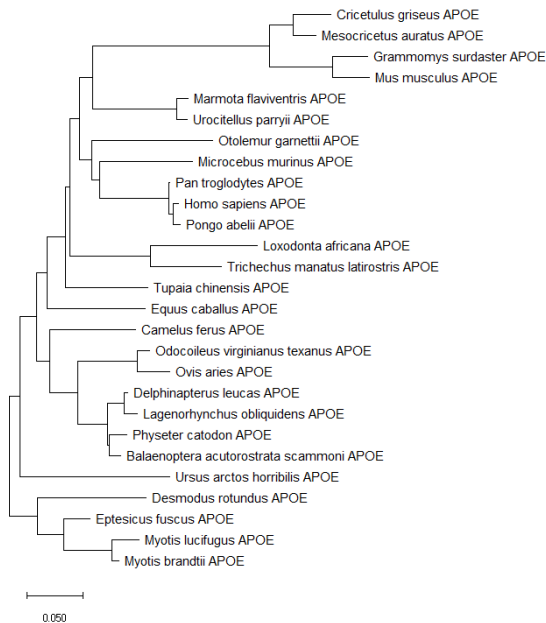


Best DNA/Protein Model (ML)

Model	Parameters	BIC	AICc	lnL	(+)	(+G)	R	$\hat{\pi}(A)$	$\hat{\pi}(T)$	$\hat{\pi}(C)$	$\hat{\pi}(G)$	$\hat{\pi}(AT)$	$\hat{\pi}(AC)$	$\hat{\pi}(AG)$	$\hat{\pi}(TA)$	$\hat{\pi}(TC)$	$\hat{\pi}(TG)$	$\hat{\pi}(CA)$	$\hat{\pi}(CT)$	$\hat{\pi}(CG)$	$\hat{\pi}(GA)$	$\hat{\pi}(GT)$	$\hat{\pi}(GC)$
HKY+G	56	10616.503	10188.211	-5037.900	n/a	0.59	1.32	0.209	0.142	0.276	0.373	0.030	0.058	0.216	0.044	0.160	0.079	0.044	0.082	0.079	0.121	0.030	0.058
HKY+G+I	57	10625.348	10189.415	-5037.495	0.13	0.83	1.32	0.209	0.142	0.276	0.373	0.030	0.058	0.216	0.044	0.160	0.079	0.044	0.082	0.079	0.121	0.030	0.058
TN93+G	57	10625.949	10190.016	-5037.795	n/a	0.59	1.32	0.209	0.142	0.276	0.373	0.030	0.058	0.221	0.044	0.154	0.079	0.044	0.079	0.079	0.123	0.030	0.058
TN93+G+I	58	10634.825	10191.252	-5037.406	0.13	0.83	1.32	0.209	0.142	0.276	0.373	0.030	0.058	0.221	0.044	0.155	0.079	0.044	0.079	0.079	0.123	0.030	0.058
T92+G	54	10642.821	10229.811	-5060.715	n/a	0.59	1.35	0.175	0.175	0.325	0.325	0.035	0.065	0.194	0.035	0.194	0.065	0.035	0.105	0.065	0.105	0.035	0.065
T92+G+I	55	10651.402	10230.751	-5060.177	0.15	0.88	1.35	0.175	0.175	0.325	0.325	0.035	0.065	0.194	0.035	0.194	0.065	0.035	0.105	0.065	0.105	0.035	0.065
GTR+G	60	10653.210	10194.356	-5036.943	n/a	0.59	1.32	0.209	0.142	0.276	0.373	0.027	0.063	0.222	0.040	0.155	0.070	0.048	0.080	0.083	0.124	0.027	0.061
GTR+G+I	61	10662.376	10195.883	-5036.698	0.11	0.78	1.33	0.209	0.142	0.276	0.373	0.028	0.063	0.222	0.041	0.155	0.070	0.048	0.080	0.082	0.124	0.027	0.061
HKY+I	56	10706.969	10278.677	-5083.133	0.38	n/a	1.29	0.209	0.142	0.276	0.373	0.030	0.059	0.214	0.045	0.158	0.080	0.045	0.081	0.080	0.120	0.030	0.059
TN93+I	57	10716.556	10280.622	-5083.099	0.38	n/a	1.29	0.209	0.142	0.276	0.373	0.030	0.059	0.212	0.045	0.161	0.080	0.045	0.083	0.080	0.118	0.030	0.059
T92+I	54	10730.078	10317.068	-5104.343	0.38	n/a	1.33	0.175	0.175	0.325	0.325	0.036	0.066	0.193	0.036	0.193	0.066	0.036	0.104	0.066	0.104	0.036	0.066
K2+G	53	10744.343	10338.975	-5116.303	n/a	0.64	1.22	0.250	0.250	0.250	0.250	0.056	0.056	0.137	0.056	0.137	0.056	0.056	0.137	0.056	0.137	0.056	0.056
GTR+I	60	10745.152	10286.298	-5082.913	0.38	n/a	1.29	0.209	0.142	0.276	0.373	0.033	0.059	0.211	0.049	0.161	0.077	0.045	0.082	0.078	0.118	0.029	0.058
K2+G+I	54	10754.000	10340.990	-5116.304	0.00	0.64	1.22	0.250	0.250	0.250	0.250	0.056	0.056	0.137	0.056	0.137	0.056	0.056	0.137	0.056	0.137	0.056	0.056
K2+I	53	10852.924	10447.555	-5170.593	0.37	n/a	1.18	0.250	0.250	0.250	0.250	0.057	0.057	0.135	0.057	0.135	0.057	0.057	0.135	0.057	0.135	0.057	0.057
JC+G	52	10881.531	10483.804	-5189.725	n/a	0.66	0.50	0.250	0.250	0.250	0.250	0.083	0.083	0.083	0.083	0.083	0.083	0.083	0.083	0.083	0.083	0.083	0.083
JC+G+I	53	10891.187	10485.818	-5189.725	0.00	0.66	0.50	0.250	0.250	0.250	0.250	0.083	0.083	0.083	0.083	0.083	0.083	0.083	0.083	0.083	0.083	0.083	0.083
JC+I	52	10985.622	10587.895	-5241.770	0.37	n/a	0.50	0.250	0.250	0.250	0.250	0.083	0.083	0.083	0.083	0.083	0.083	0.083	0.083	0.083	0.083	0.083	0.083
HKY	55	11054.866	10634.215	-5261.909	n/a	n/a	1.16	0.209	0.142	0.276	0.373	0.032	0.063	0.204	0.047	0.151	0.085	0.047	0.077	0.085	0.114	0.032	0.063
TN93	56	11062.888	10634.596	-5261.092	n/a	n/a	1.16	0.209	0.142	0.276	0.373	0.032	0.063	0.214	0.048	0.139	0.085	0.048	0.071	0.085	0.120	0.032	0.063
GTR	59	11079.174	10627.960	-5254.753	n/a	n/a	1.17	0.209	0.142	0.276	0.373	0.022	0.061	0.219	0.033	0.142	0.074	0.046	0.073	0.103	0.122	0.028	0.076

According to the best DNA/Protein Model program in MEGAX, I determined that the HKY+G model to be the best for my data set. It has the lowest BIC and AICc scores, which, when described in the textbook, the lower the score, the better. It also has the highest lnL score, meaning that the log likelihood for HKY+G is the highest amongst the models. While it has more parameters than some of the other models in the list, it appears that the BIC, AICc, and lnL scores offset the increase in parameters.

Initial Maximum Likelihood Tree:



The initial ML tree was rooted by selecting my four bat species as an outgroup.

Settings for Initial ML Tree:

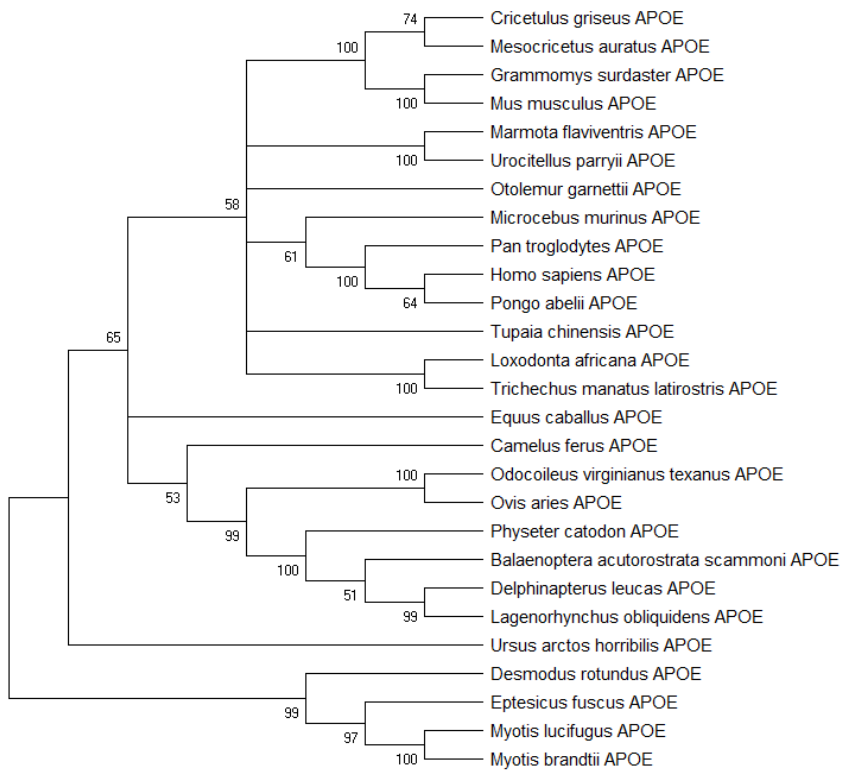
MX: Analysis Preferences

Phylogeny Reconstruction

Option	Setting
ANALYSIS	
Statistical Method →	Maximum Likelihood
PHYLOGENY TEST	
Test of Phylogeny →	None
No. of Bootstrap Replications →	Not Applicable
SUBSTITUTION MODEL	
Substitutions Type →	Nucleotide
Genetic Code Table →	Not Applicable
Model/Method →	Hasegawa-Kishino-Yano model
RATES AND PATTERNS	
Rates among Sites →	Gamma Distributed (G)
No of Discrete Gamma Categories →	5
DATA SUBSET TO USE	
Gaps/Missing Data Treatment →	Complete deletion
Site Coverage Cutoff (%) →	Not Applicable
Select Codon Positions →	<input checked="" type="checkbox"/> 1st <input checked="" type="checkbox"/> 2nd <input checked="" type="checkbox"/> 3rd <input checked="" type="checkbox"/> Noncoding Sites
TREE INFERENCE OPTIONS	
ML Heuristic Method →	Nearest-Neighbor-Interchange (NNI)
Initial Tree for ML →	Make initial tree automatically (Default - NJ/BioNJ)
Initial Tree File →	Not Applicable
Branch Swap Filter →	None
SYSTEM RESOURCE USAGE	
Number of Threads →	Not Applicable

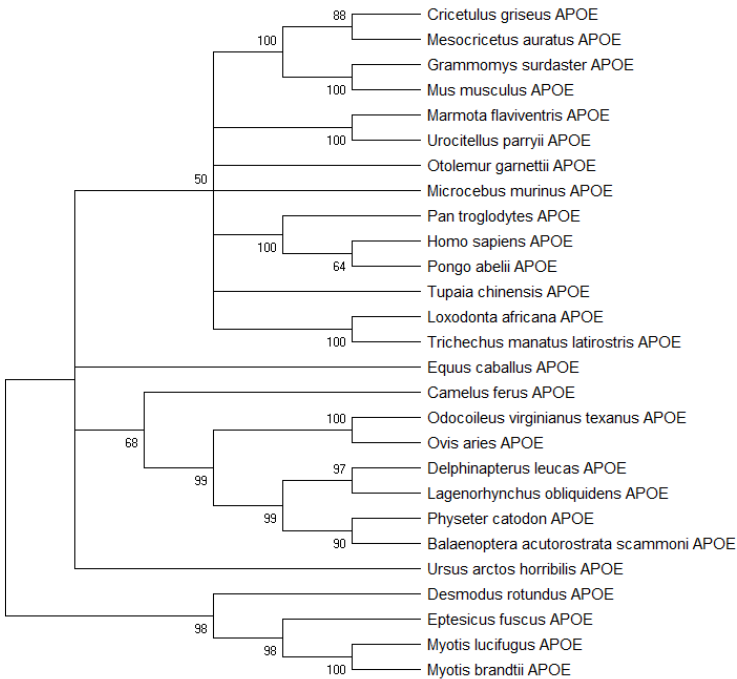
? Help ✕ Cancel ✓ OK

Consensus Maximum Likelihood Tree:



The Bootstrap consensus ML tree is rooted using my four bat species as an outgroup.

The differences between my three trees is mainly found when comparing either the MP consensus tree or the ML consensus tree to the NJ consensus tree. The MP and ML consensus trees are relatively similar in organization as well as the polytomies that have arisen after rooting the trees using my bat species. Some of the bootstrap certainties are a bit different, but the overall big picture is pretty similar between the two. The biggest difference I found was that the branch between *Ursus arctos horribilis* and the rest



of the ingroups showed 65% bootstrap confidence levels in ML, while being sub 50% in MP. The differences between NJ and both MP and ML can be seen in the amount of polytomies that have arisen in the consensus tree. Even when rooted the same as the MP and ML trees, the NJ tree does not display a similar orientation to the other two trees due to the presence of more polytomies. A trend seen in the NJ tree is that the bootstrap confidence of the branches higher than 50% are most near to 100, while in the MP and ML trees there is a bit of a range in the confidence levels.

Given that my MP and ML trees are rather similar as well as reading through Joseph's (our classmate's) post regarding Dr. Hall's testing of MP, ML, NJ, and other methods to determine their accuracy, I would hypothesize that my more accurate trees (and ones to pay attention to) are my MP and ML trees. By examining these two trees, I think I could infer that the species with the APOE gene that most closely resembles that of a human's APOE reside in the clade that homo sapiens are found in. Looking at these species, I see that they are various primates, which makes a lot of sense evolutionarily.